FIG. 1A

```
                                                    10
CCTGAAGGGAGAGAGCAGGAGGAGAGAGGAGGACAGTGGCCCAGAGAGGGCTCCTGGGCACTGGGAGG
                                                    50
                                                    70
GACGCTCTTCTTCCTGCCCAGGGTCCCTGGGCCGATGGGATCACGCAGAGAATGCCGAG
                                                    110
                                                    130
AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT
                                                    150                            M  E  L
                                                    190
GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA
                                                    210
 R  K  Y  G  P  G  R  L  A  G  T  V  I  G  G  A  A  Q  S  K
                                                    250
ATCACAGACTAAATCAGATCAATCACAAAAGAGTTCCTGCCAGCCTTTACACAGCCCC
                                                    270
 S  Q  T  K  S  D  S  I  T  K  E  F  F  L  P  G  L  Y  T  A  P
                                                    290
                                                    310
TTCCTCCCCGTTCCCGCCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT
                                                    330
 S  S  P  F  P  P  S  Q  V  S  D  H  Q  V  L  N  D  A  E  V
                                                    370
TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAACGAGAGTGACTC
                                                    390
 A  A  L  E  N  F  S  S  S  Y  D  Y  G  E  N  E  S  D  S
                                                    430
GTGCTGTACCTCCCCGCCCTGCCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT
                                                    450
 C  C  T  S  P  P  C  P  Q  D  F  S  L  N  F  D  R  A  F  L
                                                    490                            510
```

MATCH WITH FIG. 1B

MATCH WITH FIG. IA

FIG. IB

```
GCCAGCCCTCAACAGCCTCCTCTTTCTGCTGGGCGTGCTGGGCAACGGCGCCGGTGGCAGC
 P  A  L  N  S  L  L  F  L  L  G  L  L  G  N  G  A  V  A  A
          550                570                590

CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC
 V  L  L  S  R  R  T  A  L  S  S  T  D  T  F  L  L  H  L  A
          610                630                650

TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA
 V  A  D  T  L  L  V  L  T  L  P  L  W  A  V  D  A  A  V  Q
          670                690                710

GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA
 W  V  F  G  S  G  L  C  K  V  A  G  A  L  F  N  I  N  F  Y
          730                750                770

CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC
 A  G  A  L  L  L  A  C  I  S  F  D  R  Y  L  N  I  V  H  A
          790                810                830

CACCCAGCTCTACCGCCGGGGCCCCGGCCCGTGACCCTGCCACCTGGCTGTGTCTG
 T  Q  L  Y  R  R  G  P  P  A  R  V  T  L  T  C  L  A  V  W
          850                870                890

GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA
 G  L  C  L  L  F  A  L  P  D  F  I  F  L  S  A  H  H  D  E
          910                930                950

GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGCCGACGGCTCTGCG
 R  L  N  A  T  H  C  Q  Y  N  F  P  Q  V  G  R  T  A  L  R
```

MATCH WITH FIG. IC

FIG. IC

MATCH WITH FIG. IB

```
                970              990             1010
GGTGCTGCAGCTGGTGGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC
  V  L  Q  L  V  A  G  F  L  L  P  L  L  V  M  A  Y  C  Y  A
               1030             1050             1070
CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGGCCCATGCGGCT
  H  I  L  A  V  L  L  V  S  R  G  Q  R  R  L  R  A  M  R  L
               1090             1110             1130
GGTGGTGGTGGTCGTGGGCCCTTGCCCTCTGCCCCTATCACCTGGTGGTGCT
  V  V  V  V  V  A  F  A  L  C  W  T  P  Y  H  L  V  V  L
               1150             1170             1190
GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT
  V  D  I  L  M  D  L  G  A  L  A  R  N  C  G  R  E  S  R  V
               1210             1230             1250
AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT
  D  V  A  K  S  V  T  S  G  L  G  Y  M  H  C  C  L  N  P  L
               1270             1290             1310
GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT
  L  Y  A  F  V  G  V  K  F  R  E  R  M  W  M  L  L  L  R  L
```

MATCH WITH FIG. ID

MATCH WITH FIG. IC   FIG. ID

```
                         1330              1350              1370
GGGCTGCCCAACCAGAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCGGGATTCATC
 G   C   P   N   Q   R   G   L   Q   R   Q   P   S   S   R   D   S   S
                         1390              1410              1430
CTGGTCTGAGACCTTCAGAGGCCTTCCTACTCGGGCTTGTGAGGCCGAATCCGGGCTCCCC
 W   S   E   T   S   E   A   S   Y   S   G   L   *
                         1450              1470              1490
TTTCGGCCCACAGTCTGACTTCCCCGGCCATTCCCAGGCTCCTCCCCTCTGCGGCTCTGG
                         1510              1530              1550
CTCTCCCCAATATCCTGCGTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC
                         1570              1590              1610
GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC
                         1630              1650              1670
CATCCTCTGCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA
                         1690              1710              1730
ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCCGTAGAGGGTGCTGCCCCATGA
                         1750              1770              1790
AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCCTCTAT
                         1810              1830              1850
ATTTGGTCTTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG
                         1870
TCAGGAAAAAAAAAA
```

09/101518

FIG. 2A

```
 54 DHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFL 103
  2 ...ESDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPCEPE......SLEINKYFV 46

104 PALNSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTL 153
 47 VIIYALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTL 96

154 PLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLACISFDRYLNIVHA 203
 97 PIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLACISVDRYLAIVHA 146

204 TQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYN 253
147 TRTLTQ.KRYLVKFICLSIWGLSLLLALPVLLFRRTVYSSNVSPACYEDM 195

254 FPQVG..RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAM 301
196 GNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQKHRAM 245
```

MATCH WITH FIG. 2B

FIG. 2B

MATCH WITH FIG. 2A

```
302 RLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
         : :  |||| ||.:|||  .    .    .   .     .
246 RVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE 295

352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRD 401
     .  :|| ||||||||.| ||| ||  .:. : |  . .   . : : :.
296 ILGILHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVG 345

402 SSWSETSEA 410
     :  .  |:..
346 SSSGHTSTT 354
```